

What is claimed is:

1. A plant expression cassette, which comprises  
a glutamine synthetase gene coding sequence operably  
5 linked to a promoter.

2. The expression cassette of claim 1, wherein  
the glutamine synthetase coding sequence is from a  
gymnosperm.

10 3. The expression cassette of claim 2, wherein  
the glutamine synthetase coding sequence is from the  
genus *Pinus*.

15 4. The expression cassette of claim 3, wherein  
the glutamate synthetase coding sequence is from *Pinus*  
*sylvestris*.

20 5. The expression cassette of claim 2, in which  
the promoter is the cauliflower mosaic virus 35S  
promoter.

25 6. The expression cassette of claim 5, which  
further comprises the NOS terminator sequence operably  
linked to the glutamine synthetase coding sequence.

7. The expression cassette of claim 1, which is  
contains a nucleic acid sequence selected from the group  
consisting of:

30 A.) a nucleic acid sequence that is at least  
70% identical to Genbank Accession No. X69822;

B.) a nucleic acid sequence that encodes a  
protein that is at least 70% similar to Genbank Accession  
No. X69822;

C.) a nucleic acid sequence that hybridizes to Genbank Accession No. X69822 at moderate stringency; and

D.) a nucleic acid sequence that is Genbank Accession No. X69822.

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8. A vector, comprising the expression cassette of claim 1.

9. The vector of claim 8, which is an *Agrobacterium* binary vector.

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10. The vector of claim 9, wherein the vector is pBIN19.

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11. The vector of claim 10, which further comprises the neomycin phosphotransferase II coding sequence.

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<sup>Sub</sup>  
<sup>acc</sup> 12. A method of producing a plant with improved nitrogen metabolism by transforming in vitro said plant with the expression cassette of claim 1.

13. The method of claim 12, wherein the plant is a woody perennial.

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14. The method of claim 13, wherein the plant is in the family *Salicaceae*.

15. The method of claim 14, wherein the plant is in the genus *Populus*.

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<sup>Sub</sup>  
<sup>acc</sup> 16. The method of claim 15, wherein the plant is the hybrid *Populus tremula* X *P. alba*.

17. The method of claim 16, wherein the plant is clone INRA 717 1-B4 of hybrid *Populus tremula* X *P. alba*.

5 18. The method of claim 12, wherein the transformation step uses the *Agrobacterium tumefaciens* method.

10 19. The method of claim 13, wherein the transformation step further uses the vector of claim 9.

20. A transgenic plant produced by the method of claim 12.

15 21. A reproductive unit from the transgenic plant of claim 15.

21. 22. A cell from the transgenic plant of claim 21.

20 23. A transgenic plant with an improved nitrogen metabolism, which is a woody perennial and comprises at least one transgene that comprises the coding sequence of a glutamine synthetase gene.

25 24. The transgenic plant of claim 23, wherein the glutamine synthetase gene is from a gymnosperm.

30 25. The transgenic plant of claim 24, wherein the glutamine synthetase genes is from *Pinus sylvestris*.

26. The transgenic plant of claim 25, wherein the glutamine synthetase coding sequence is Genbank Accession No. X69822.

27. The transgenic plant of claim 17, which is from the family Salicaceae.

5 28. The transgenic plant of claim 23, which is from the genus *Populus*.

29. The transgenic plant of claim 28, which is a hybrid of *Populus tremula* X *Populus alba*.

10 30. The transgenic plant of claim 29, which is clone INRA 717 1-B4 of the hybrid *Populus tremula* X *Populus alba*.

15 31. A reproductive unit from the transgenic plant of claim 23.

20 32. A transgenic plant, which is a woody perennial, and exhibits a growth rate that is statistically significantly greater at the  $P=0.05$  level than that of equivalent untransformed plants.

25 33. The transgenic plant of claim 32, which additionally exhibits a protein concentration in gram per gram fresh weight in the mature leaves that is statistically significantly greater at the  $P=0.05$  level than that of mature leaves in equivalent untransformed plants.

30 34. The transgenic plant of claim 33, which additionally exhibits a chlorophyll concentration in gram per gram fresh weight in the mature leaves that is statistically significantly greater at the  $P=0.05$  level than that of mature leaves in equivalent untransformed plants.

35. The transgenic plant of claim 34, which additionally exhibits a mature leaf area in  $\text{cm}^2$  per leaf that is statistically significantly greater at the  $P=0.05$  level than that of mature leaves in equivalent  
5 untransformed plants.

36. The transgenic plant of claim 32, which is from the family Salicaceae.

10 37. The transgenic plant of claim 36, which is from the genus *Populus*.

38. The transgenic plant of claim 37, which is a hybrid of *Populus tremula* X *Populus alba*.  
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39. The transgenic plant of claim 38, which is clone INRA 717 1-B4 of the hybrid *Populus tremula* X *Populus alba*.

20 40. A reproductive unit from the transgenic plant of claim 32.